

ctc cgg tcc aag aag gct gtt gac tgg cgt ctc ttt cgt aac att ttt 2033

Leu Arg Ser Lys Lys Ala Val Asp Trp Arg Leu Phe Arg Asn Ile Phe

640

645

650

atg gcc tgg ttt gtc aca gtc cct att tct gga gtt atc agt gct gcc 2081

Met Ala Trp Phe Val Thr Val Pro Ile Ser Gly Val Ile Ser Ala Ala

655

660

665

atc atg gca atc ttc aga tat gtc atc ctc aga atg tgaagctgtt 2127

Ile Met Ala Ile Phe Arg Tyr Val Ile Leu Arg Met

670

675

tgagattaaa atttgtgtca atgtttggga ccattctagg tattcctgct cccctgaaga 2187

atgattacag tgttaacaga agactgacaa gagtcctttt atttgggagc cagaggaggg 2247

aagtgttact tgtgctataa ctgcttttgt gctaaatatg aattgtctca aaattagctg 2307

tgtaaaatag cccgggttcc actggctcct gctgaggtcc cctttccttc tgggctgtga 2367

attcctgtac atatttctct actttttgta tcaggcttca attccattat gttttaatgt 2427

tgtctctgaa gatgacttgt gatttttttt tctttttttt aaaccatgaa gagccgtttg 2487

acagagcatg ctctgcgttg ttggtttcac cagcttctgc cctcacatgc acagggattt 2547

aacaacaaaa atataactac aacttccctt gtagtctctt atataagtag agtccttggt 2607

actctgccct cctgtcagta gtggcaggat ctattggcat attcgggagc ttcttagagg 2667

gatgaggttc tttgaacaca gtgaaaattt aaattagtaa cttttttgca agcagtttat 2727

tgactgttat tgctaagaag aagtaagaaa gaaaaagcct gttggcaatc ttggttattt 2787

ctttaagatt tctggcagtg tgggatgat gaatgaagtg gaatgtgaac tttgggcaag 2847

ttaaattggga cagccttcca tgttcatttg tctacctctt aactgaataa aaaagcctac 2907

agtttttag 2916

<210> 125

<211> 288

<212> PRT

<213> Homo sapiens

<400> 125

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln Asp Leu Ser Glu Ala

1 5 10 15

Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln Ala Glu Asn Ala Glu

20 25 30

Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr Arg Asp Gly Phe Lys

35 40 45

Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val Ala Leu Glu Glu Glu

50 55 60

Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala Pro Val Tyr Phe Pro
65 70 75 80

Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln Asp Leu Ala Phe Trp
85 90 95

Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr Thr Pro Ala Met Gln
100 105 110

Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg Thr Glu Pro Glu Leu
115 120 125

Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly Asp Leu Ser Gly Gly
130 135 140

Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu Asp Leu Pro Ser Ser
145 150 155 160

Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn Ile Ala Ser Ala Thr
165 170 175

Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn Ser Leu Glu Met Thr
180 185 190

Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala Lys Thr Ala Phe Leu
195 200 205

Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu Leu Leu Thr His Asp

210

215

220

Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly Leu Arg Gln Arg Ala

225

230

235

240

Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu Thr Pro Arg Gly Lys

245

250

255

Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu Leu Arg Trp Val Leu

260

265

270

Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val Gly Leu Tyr Ala Met

275

280

285

<210> 126

<211> 1550

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (81)..(944)

<400> 126

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acgagcccag caccggccgg atg gag cgt ccg caa ccc gac agc atg ccc cag 113

Met Glu Arg Pro Gln Pro Asp Ser Met Pro Gln

1

5

10

gat ttg tca gag gcc ctg aag gag gcc acc aag gag gtg cac acc cag 161

Asp Leu Ser Glu Ala Leu Lys Glu Ala Thr Lys Glu Val His Thr Gln

15

20

25

gca gag aat gct gag ttc atg agg aac ttt cag aag ggc cag gtg acc 209

Ala Glu Asn Ala Glu Phe Met Arg Asn Phe Gln Lys Gly Gln Val Thr

30

35

40

cga gac ggc ttc aag ctg gtg atg gcc tcc ctg tac cac atc tat gtg 257

Arg Asp Gly Phe Lys Leu Val Met Ala Ser Leu Tyr His Ile Tyr Val

45

50

55

gcc ctg gag gag gag att gag cgc aac aag gag agc cca gtc ttc gcc 305

Ala Leu Glu Glu Glu Ile Glu Arg Asn Lys Glu Ser Pro Val Phe Ala

60

65

70

75

cct gtc tac ttc cca gaa gag ctg cac cgc aag gct gcc ctg gag cag 353

Pro Val Tyr Phe Pro Glu Glu Leu His Arg Lys Ala Ala Leu Glu Gln

80

85

90

gac ctg gcc ttc tgg tac ggg ccc cgc tgg cag gag gtc atc ccc tac 401

Asp Leu Ala Phe Trp Tyr Gly Pro Arg Trp Gln Glu Val Ile Pro Tyr

95

100

105

aca cca gcc atg cag cgc tat gtg aag cgg ctc cac gag gtg ggg cgc 449

Thr Pro Ala Met Gln Arg Tyr Val Lys Arg Leu His Glu Val Gly Arg

110

115

120

aca gag ccc gag ctg ctg gtg gcc cac gcc tac acc cgc tac ctg ggt 497

Thr Glu Pro Glu Leu Leu Val Ala His Ala Tyr Thr Arg Tyr Leu Gly

125

130

135

gac ctg tct ggg ggc cag gtg ctc aaa aag att gcc cag aaa gcc ctg 545

Asp Leu Ser Gly Gly Gln Val Leu Lys Lys Ile Ala Gln Lys Ala Leu

140

145

150

155

gac ctg ccc agc tct ggc gag ggc ctg gcc ttc ttc acc ttc ccc aac 593

Asp Leu Pro Ser Ser Gly Glu Gly Leu Ala Phe Phe Thr Phe Pro Asn

160

165

170

att gcc agt gcc acc aag ttc aag cag ctc tac cgc tcc cgc atg aac 641

Ile Ala Ser Ala Thr Lys Phe Lys Gln Leu Tyr Arg Ser Arg Met Asn

175

180

185

tcc ctg gag atg act ccc gca gtc agg cag agg gtg ata gaa gag gcc 689

Ser Leu Glu Met Thr Pro Ala Val Arg Gln Arg Val Ile Glu Glu Ala

190

195

200

aag act gcg ttc ctg ctc aac atc cag ctc ttt gag gag ttg cag gag 737

Lys Thr Ala Phe Leu Leu Asn Ile Gln Leu Phe Glu Glu Leu Gln Glu

205

210

215

ctg ctg acc cat gac acc aag gac cag agc ccc tca cgg gca cca ggg 785

Leu Leu Thr His Asp Thr Lys Asp Gln Ser Pro Ser Arg Ala Pro Gly

220

225

230

235

ctt cgc cag cgg gcc agc aac aaa gtg caa gat tct gcc ccc gtg gag 833
Leu Arg Gln Arg Ala Ser Asn Lys Val Gln Asp Ser Ala Pro Val Glu

240

245

250

act ccc aga ggg aag ccc cca ctc aac acc cgc tcc cag gct ccg ctt 881
Thr Pro Arg Gly Lys Pro Pro Leu Asn Thr Arg Ser Gln Ala Pro Leu

255

260

265

ctc cga tgg gtc ctt aca ctc agc ttt ctg gtg gcg aca gtt gct gta 929
Leu Arg Trp Val Leu Thr Leu Ser Phe Leu Val Ala Thr Val Ala Val

270

275

280

ggg ctt tat gcc atg tgaatgcagg catgctggct cccagggcca tgaactttgt 984
Gly Leu Tyr Ala Met

285

ccggtggaag gccttctttc tagagaggga attctcttgg ctggttccct taccgtgggc 1044

actgaaggct ttcagggcct ccagccctct cactgtgtcc ctctctctgg aaaggaggaa 1104

ggagcctatg gcattctccc caacgaaaag cacatccagg caatggccta aacttcagag 1164

ggggcgaagg ggtcagccct gcccttcagc atcctcagtt cctgcagcag agcctggaag 1224

acacccta atgtggcagctg tctcaaacct ccaaaagccc tgagtttcaa gtatccttgt 1284

tgacacggcc atgaccactt tccccgtggg ccatggcaat ttttacacaa acctgaaaag 1344

atgttgtgtc ttgtgttttt gtcttatttt tgttgagacc actctgttcc tggtcagcc 1404

tcaaatgcag tatttttgtt gtgttctgtt gtttttatag cagggttggg gtggtttttg 1464

agccatgcgt ggggtggggag ggaggtgttt aacggcactg tggccttggt ctaacttttg 1524

tgtgaaataa taaacaacat tgtctg 1550

<210> 127

<211> 135

<212> PRT

<213> Homo sapiens

<400> 127

Met Ala Cys Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu

1 5 10 15

Cys Leu Arg Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val

20 25 30

Leu Asn Leu Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro

35 40 45

Arg Phe Asn Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys

50 55 60

Asp Gly Gly Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe

65 70 75 80

Gln Pro Gly Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn

85

90

95

Leu Thr Val Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg

100

105

110

Leu Asn Leu Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys

115

120

125

Ile Lys Cys Val Ala Phe Asp

130

135

<210> 128

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (50)..(454)

<400> 128

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Met Ala Cys

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ggt ctg gtc gcc agc aac ctg aat ctc aaa cct gga gag tgc ctt cga 106

Gly Leu Val Ala Ser Asn Leu Asn Leu Lys Pro Gly Glu Cys Leu Arg

5

10

15

gtg cga ggc gag gtg gct cct gac gct aag agc ttc gtg ctg aac ctg 154

Val Arg Gly Glu Val Ala Pro Asp Ala Lys Ser Phe Val Leu Asn Leu

20

25

30

35

ggc aaa gac agc aac aac ctg tgc ctg cac ttc aac cct cgc ttc aac 202

Gly Lys Asp Ser Asn Asn Leu Cys Leu His Phe Asn Pro Arg Phe Asn

40

45

50

gcc cac ggc gac gcc aac acc atc gtg tgc aac agc aag gac ggc ggc 250

Ala His Gly Asp Ala Asn Thr Ile Val Cys Asn Ser Lys Asp Gly Gly

55

60

65

gcc tgg ggc acc gag cag cgg gag gct gtc ttt ccc ttc cag cct gga 298

Ala Trp Gly Thr Glu Gln Arg Glu Ala Val Phe Pro Phe Gln Pro Gly

70

75

80

agt gtt gca gag gtg tgc atc acc ttc gac cag gcc aac ctg acc gtc 346

Ser Val Ala Glu Val Cys Ile Thr Phe Asp Gln Ala Asn Leu Thr Val

85

90

95

aag ctg cca gat gga tac gaa ttc aag ttc ccc aac cgc ctc aac ctg 394

Lys Leu Pro Asp Gly Tyr Glu Phe Lys Phe Pro Asn Arg Leu Asn Leu

100

105

110

115

gag gcc atc aac tac atg gca gct gac ggt gac ttc aag atc aaa tgt 442

Glu Ala Ile Asn Tyr Met Ala Ala Asp Gly Asp Phe Lys Ile Lys Cys

120

125

130

gtg gcc ttt gac tgaaatcagc cagcccatgg cccccaataa aggcagctgc 494

Val Ala Phe Asp

135

ctctgctccc ctg 507

<210> 129

<211> 662

<212> PRT

<213> Homo sapiens

<400> 129

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn

1

5

10

15

Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn

20

25

30

Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp

35

40

45

Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys

50

55

60

Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser

65

70

75

80

Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr
85 90 95

Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu
100 105 110

Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys
115 120 125

His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile
130 135 140

Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp Glu Leu
145 150 155 160

Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro
165 170 175

Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn Tyr Arg
180 185 190

Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu Leu Thr
195 200 205

Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu Asp Leu
210 215 220

Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu
225 230 235 240

Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly Tyr Glu
 245 250 255

Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn Pro Tyr
 260 265 270

Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu Met Gln
 275 280 285

Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys Arg Lys
 290 295 300

Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val
 305 310 315 320

Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala
 325 330 335

Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe
 340 345 350

Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu Leu Asp
 355 360 365

Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln
 370 375 380

Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp

400

Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu

415

Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu Lys Phe

430

Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe Ser Asn

445

Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile

460

Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp

480

Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu

495

Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser

510

Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr

525

Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn

540

Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly Leu Gly
545 550 555 560

Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro Tyr Gln
565 570 575

Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln
580 585 590

Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn
595 600 605

Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe
610 615 620

Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg Ser Asn
625 630 635 640

Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg
645 650 655

Leu Arg Ile Ser Glu Lys
660

<210> 130

<211> 2251

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)..(2059)

<400> 130

cttggctgga cagtttgtga aactgtgttg ccgggcaact ggacatcctt ttgttcaata 60

tcagtggttc aaa atg aat aaa gag att cca aat gga aat aca tca gag 109

Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu

1

5

10

ctt att ttt aat gca gtg cat gta aaa gat gca ggc ttt tat gtc tgt 157

Leu Ile Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys

15

20

25

cga gtt aat aac aat ttc acc ttt gaa ttc agc cag tgg tca cag ctg 205

Arg Val Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu

30

35

40

gat gtt tgc gac atc cca gag agc ttc cag aga agt gtt gat ggc gtc 253

Asp Val Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val

45

50

55

60

tct gaa tcc aag ttg caa atc tgt gtt gaa cca act tcc caa aag ctg 301

Ser Glu Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu

65

70

75

atg cca ggc agc aca ttg gtt tta cag tgt gtt gct gtt gga agc cct 349

Met Pro Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro

80

85

90

att cct cac tac cag tgg ttc aaa aat gaa tta cca tta aca cat gag 397

Ile Pro His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu

95

100

105

acc aaa aag cta tac atg gtg cct tat gtg gat ttg gaa cac caa gga 445

Thr Lys Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly

110

115

120

acc tac tgg tgt cat gta tat aat gat cga gac agt caa gat agc aag 493

Thr Tyr Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys

125

130

135

140

aag gta gaa atc atc ata gga aga aca gat gag gca gtg gag tgc act 541

Lys Val Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr

145

150

155

gaa gat gaa tta aat aat ctt ggt cat cct gat aat aaa gag caa aca 589

Glu Asp Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr

160

165

170

act gac cag cct ttg gcg aag gac aag gtt gcc ctt ttg ata gga aat 637

Thr Asp Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn

175

180

185

atg aat tac cgg gag cac ccc aag ctc aaa gct cct ttg gtg gat gtg 685

Met Asn Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val

190

195

200

tac gaa ttg act aac tta ctg aga cag ctg gac ttc aaa gtg gtt tca 733

Tyr Glu Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser

205

210

215

220

ctg ttg gat ctt act gaa tat gag atg cgt aat gct gtg gat gag ttt 781

Leu Leu Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe

225

230

235

tta ctc ctt tta gac aag gga gta tat ggg tta tta tat tat gca gga 829

Leu Leu Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly

240

245

250

cat ggt tat gaa aat ttt ggg aac agc ttc atg gtc ccc gtt gat gct 877

His Gly Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala

255

260

265

cca aat cca tat agg tct gaa aat tgt ctg tgt gta caa aat ata ctg 925

Pro Asn Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu

270

275

280

aaa ttg atg caa gaa aaa gaa act gga ctt aat gtg ttc tta ttg gat 973

Lys Leu Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp

285

290

295

300

atg tgt agg aaa aga aat gac tac gat gat acc att cca atc ttg gat 1021

Met Cys Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp

305

310

315

gca cta aaa gtc acc gcc aat att gtg ttt gga tat gcc acg tgt caa 1069

Ala Leu Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln

320

325

330

gga gca gaa gct ttt gaa atc cag cat tct gga ttg gca aat gga atc 1117

Gly Ala Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile

335

340

345

ttt atg aaa ttt tta aaa gac aga tta tta gaa gat aag aaa atc act 1165

Phe Met Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr

350

355

360

gtg tta ctg gat gaa gtt gca gaa gat atg ggt aag tgt cac ctt acc 1213

Val Leu Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr

365

370

375

380

aaa ggc aaa cag gct cta gag att cga agt agt tta tct gag aag aga 1261

Lys Gly Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg

385

390

395

gca ctt act gat cca ata cag gga aca gaa tat tct gct gaa tct ctt 1309

Ala Leu Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu

400

405

410

gtg cgg aat cta cag tgg gcc aag gct cat gaa ctt cca gaa agt atg 1357

Val Arg Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met

415

420

425

tgt ctt aag ttt gac tgt ggt gtt cag att caa tta gga ttt gca gct 1405

Cys Leu Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala

430

435

440

gag ttt tcc aat gtc atg atc atc tat aca agt ata gtt tac aaa cca 1453

Glu Phe Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro

445

450

455

460

ccg gag ata ata atg tgt gat gcc tac gtt act gat ttt cca ctt gat 1501

Pro Glu Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp

465

470

475

cta gat att gat cca aaa gat gca aat aaa ggc aca cct gaa gaa act 1549

Leu Asp Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr

480

485

490

ggc agc tac ttg gta tca aag gat ctt ccc aag cat tgc ctc tat acc 1597

Gly Ser Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr

495

500

505

aga ctc agt tca ctg caa aaa tta aag gaa cat cta gtc ttc aca gta 1645

Arg Leu Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val

510

515

520

tgt tta tca tat cag tac tca gga ttg gaa gat act gta gag gac aag 1693

Cys Leu Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys

525

530

535

540

cag gaa gtg aat gtt ggg aaa cct ctc att gct aaa tta gac atg cat 1741

Gln Glu Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His

545

550

555

cga ggt ttg gga agg aag act tgc ttt caa act tgt ctt atg tct aat 1789

Arg Gly Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn

560

565

570

ggt cct tac cag agt tct gca gcc acc tca gga gga gca ggg cat tat 1837

Gly Pro Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr

575

580

585

cac tca ttg caa gac cca ttc cat ggt gtt tac cat tca cat cct ggt 1885

His Ser Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly

590

595

600

aat cca agt aat gtt aca cca gca gat agc tgt cat tgc agc cgg act 1933

Asn Pro Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr

605

610

615

620

cca gat gca ttt att tca agt ttc gct cac cat gct tca tgt cat ttt 1981

Pro Asp Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe

625

630

635

agt aga agt aat gtg cca gta gag aca act gat gaa ata cca ttt agt 2029

Ser Arg Ser Asn Val Pro Val Glu Thr Thr Asp Glu Ile Pro Phe Ser

640

645

650

ttc tct gac agg ctc aga att tct gaa aaa tgacctcctt gtttttgaaa 2079

Phe Ser Asp Arg Leu Arg Ile Ser Glu Lys

655

660

g t t a g c a t a a t t t t a g a t g c c t g t g a a a t a g t a c t g c a c t t a c a t a a a g t g a g a c a t t g t 2139

g a a a a g g c a a a t t t g t a t a t g t a g a g a a g a a t a g t a g t a a c t g t t t c a t a g c a a a c t t c 2199

a g g a c t t t g a g a t g t t g a a a t t a c a t t a t t t a a t t a c a g a c t t c c t c t t t c t 2251

<210> 131

<211> 824

<212> PRT

<213> Homo sapiens

<400> 131

Met Ser Leu Leu Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala

1

5

10

15

Pro Thr Gly Pro Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg

20

25

30

Leu Arg Glu Pro Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala

35

40

45

Pro Glu Gly Arg Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg

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Gly Arg Leu Arg Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys

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Val Leu Glu Pro Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met

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90

95

Gly Glu Lys Gly Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala

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105

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Met Glu His Thr Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys

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Ile Thr Val Asn Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val

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Lys Leu Cys Cys Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp

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Phe Lys Met Asn Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile

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Phe Asn Ala Val His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val

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Asn Asn Asn Phe Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val

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Cys Asp Ile Pro Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu

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215

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Ser Lys Leu Gln Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro

225 230 235 240

Gly Ser Thr Leu Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro

245 250 255

His Tyr Gln Trp Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys

260 265 270

Lys Leu Tyr Met Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr

275 280 285

Trp Cys His Val Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val

290 295 300

Glu Ile Ile Ile Gly Arg Thr Asp Glu Ala Val Glu Cys Thr Glu Asp

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Glu Leu Asn Asn Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp

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Gln Pro Leu Ala Lys Asp Lys Val Ala Leu Leu Ile Gly Asn Met Asn

340 345 350

Tyr Arg Glu His Pro Lys Leu Lys Ala Pro Leu Val Asp Val Tyr Glu

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Leu Thr Asn Leu Leu Arg Gln Leu Asp Phe Lys Val Val Ser Leu Leu

370 375 380

Asp Leu Thr Glu Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu
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Leu Leu Asp Lys Gly Val Tyr Gly Leu Leu Tyr Tyr Ala Gly His Gly
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Tyr Glu Asn Phe Gly Asn Ser Phe Met Val Pro Val Asp Ala Pro Asn
 420 425 430

Pro Tyr Arg Ser Glu Asn Cys Leu Cys Val Gln Asn Ile Leu Lys Leu
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Met Gln Glu Lys Glu Thr Gly Leu Asn Val Phe Leu Leu Asp Met Cys
 450 455 460

Arg Lys Arg Asn Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu
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Lys Val Thr Ala Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala
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Glu Ala Phe Glu Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met
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Lys Phe Leu Lys Asp Arg Leu Leu Glu Asp Lys Lys Ile Thr Val Leu
 515 520 525

Leu Asp Glu Val Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly
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Lys Gln Ala Leu Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu
545 550 555 560

Thr Asp Pro Ile Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg
565 570 575

Asn Leu Gln Trp Ala Lys Ala His Glu Leu Pro Glu Ser Met Cys Leu
580 585 590

Lys Phe Asp Cys Gly Val Gln Ile Gln Leu Gly Phe Ala Ala Glu Phe
595 600 605

Ser Asn Val Met Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu
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Ile Ile Met Cys Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp
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Ile Asp Pro Lys Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser
645 650 655

Tyr Leu Val Ser Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu
660 665 670

Ser Ser Leu Gln Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu
675 680 685

Ser Tyr Gln Tyr Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu

690

695

700

Val Asn Val Gly Lys Pro Leu Ile Ala Lys Leu Asp Met His Arg Gly

705

710

715

720

Leu Gly Arg Lys Thr Cys Phe Gln Thr Cys Leu Met Ser Asn Gly Pro

725

730

735

Tyr Gln Ser Ser Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser

740

745

750

Leu Gln Asp Pro Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro

755

760

765

Ser Asn Val Thr Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp

770

775

780

Ala Phe Ile Ser Ser Phe Ala His His Ala Ser Cys His Phe Ser Arg

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Met Ser Leu Leu

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ggg gac ccg cta cag gcc ctg ccg ccc tcg gcc gcc ccc acg ggg ccg 224

Gly Asp Pro Leu Gln Ala Leu Pro Pro Ser Ala Ala Pro Thr Gly Pro

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ctg ctc gcc cct ccg gcc ggc gcg acc ctc aac cgc ctg cgg gag ccg 272

Leu Leu Ala Pro Pro Ala Gly Ala Thr Leu Asn Arg Leu Arg Glu Pro

25

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ctg ctg cgg agg ctc agc gag ctc ctg gat cag gcg ccc gag ggc cgg 320

Leu Leu Arg Arg Leu Ser Glu Leu Leu Asp Gln Ala Pro Glu Gly Arg

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ggc tgg agg aga ctg gcg gag ctg gcg ggg agt cgc ggg cgc ctc cgc 368

Gly Trp Arg Arg Leu Ala Glu Leu Ala Gly Ser Arg Gly Arg Leu Arg

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ctc agt tgc cta gac ctg gag cag tgt tct ctt aag gta ctg gag cct 416

Leu Ser Cys Leu Asp Leu Glu Gln Cys Ser Leu Lys Val Leu Glu Pro

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gaa gga agc ccc agc ctg tgt ctg ctg aag tta atg ggt gaa aaa ggt 464

Glu Gly Ser Pro Ser Leu Cys Leu Leu Lys Leu Met Gly Glu Lys Gly

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95

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tgc aca gtc aca gaa ttg agt gat ttc ctg cag gct atg gaa cac act 512

Cys Thr Val Thr Glu Leu Ser Asp Phe Leu Gln Ala Met Glu His Thr

105

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gaa gtt ctt cag ctt ctc agc ccc cca gga ata aag att act gta aac 560

Glu Val Leu Gln Leu Leu Ser Pro Pro Gly Ile Lys Ile Thr Val Asn

120

125

130

cca gag tca aag gca gtc ttg gct gga cag ttt gtg aaa ctg tgt tgc 608

Pro Glu Ser Lys Ala Val Leu Ala Gly Gln Phe Val Lys Leu Cys Cys

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cgg gca act gga cat cct ttt gtt caa tat cag tgg ttc aaa atg aat 656

Arg Ala Thr Gly His Pro Phe Val Gln Tyr Gln Trp Phe Lys Met Asn

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aaa gag att cca aat gga aat aca tca gag ctt att ttt aat gca gtg 704

Lys Glu Ile Pro Asn Gly Asn Thr Ser Glu Leu Ile Phe Asn Ala Val

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cat gta aaa gat gca ggc ttt tat gtc tgt cga gtt aat aac aat ttc				752
His Val Lys Asp Ala Gly Phe Tyr Val Cys Arg Val Asn Asn Asn Phe				
	185	190	195	
acc ttt gaa ttc agc cag tgg tca cag ctg gat gtt tgc gac atc cca				800
Thr Phe Glu Phe Ser Gln Trp Ser Gln Leu Asp Val Cys Asp Ile Pro				
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gag agc ttc cag aga agt gtt gat ggc gtc tct gaa tcc aag ttg caa				848
Glu Ser Phe Gln Arg Ser Val Asp Gly Val Ser Glu Ser Lys Leu Gln				
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atc tgt gtt gaa cca act tcc caa aag ctg atg cca ggc agc aca ttg				896
Ile Cys Val Glu Pro Thr Ser Gln Lys Leu Met Pro Gly Ser Thr Leu				
	230	235	240	
gtt tta cag tgt gtt gct gtt gga agc cct att cct cac tac cag tgg				944
Val Leu Gln Cys Val Ala Val Gly Ser Pro Ile Pro His Tyr Gln Trp				
245	250	255	260	
ttc aaa aat gaa tta cca tta aca cat gag acc aaa aag cta tac atg				992
Phe Lys Asn Glu Leu Pro Leu Thr His Glu Thr Lys Lys Leu Tyr Met				
	265	270	275	
gtg cct tat gtg gat ttg gaa cac caa gga acc tac tgg tgt cat gta				1040
Val Pro Tyr Val Asp Leu Glu His Gln Gly Thr Tyr Trp Cys His Val				
	280	285	290	

tat aat gat cga gac agt caa gat agc aag aag gta gaa atc atc ata 1088

Tyr Asn Asp Arg Asp Ser Gln Asp Ser Lys Lys Val Glu Ile Ile Ile

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Leu Gly His Pro Asp Asn Lys Glu Gln Thr Thr Asp Gln Pro Leu Ala

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aag gac aag gtt gcc ctt ttg ata gga aat atg aat tac cgg gag cac 1232

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ccc aag ctc aaa gct cct ttg gtg gat gtg tac gaa ttg act aac tta 1280

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Tyr Glu Met Arg Asn Ala Val Asp Glu Phe Leu Leu Leu Leu Asp Lys

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Asp Tyr Asp Asp Thr Ile Pro Ile Leu Asp Ala Leu Lys Val Thr Ala

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aat att gtg ttt gga tat gcc acg tgt caa gga gca gaa gct ttt gaa 1664

Asn Ile Val Phe Gly Tyr Ala Thr Cys Gln Gly Ala Glu Ala Phe Glu

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atc cag cat tct gga ttg gca aat gga atc ttt atg aaa ttt tta aaa 1712

Ile Gln His Ser Gly Leu Ala Asn Gly Ile Phe Met Lys Phe Leu Lys

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gac aga tta tta gaa gat aag aaa atc act gtg tta ctg gat gaa gtt 1760

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520 525 530

gca gaa gat atg ggt aag tgt cac ctt acc aaa ggc aaa cag gct cta 1808
Ala Glu Asp Met Gly Lys Cys His Leu Thr Lys Gly Lys Gln Ala Leu
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gag att cga agt agt tta tct gag aag aga gca ctt act gat cca ata 1856
Glu Ile Arg Ser Ser Leu Ser Glu Lys Arg Ala Leu Thr Asp Pro Ile
550 555 560

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Gln Gly Thr Glu Tyr Ser Ala Glu Ser Leu Val Arg Asn Leu Gln Trp
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585 590 595

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Ile Ile Tyr Thr Ser Ile Val Tyr Lys Pro Pro Glu Ile Ile Met Cys
615 620 625

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Asp Ala Tyr Val Thr Asp Phe Pro Leu Asp Leu Asp Ile Asp Pro Lys

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gat gca aat aaa ggc aca cct gaa gaa act ggc agc tac ttg gta tca 2144

Asp Ala Asn Lys Gly Thr Pro Glu Glu Thr Gly Ser Tyr Leu Val Ser

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aag gat ctt ccc aag cat tgc ctc tat acc aga ctc agt tca ctg caa 2192

Lys Asp Leu Pro Lys His Cys Leu Tyr Thr Arg Leu Ser Ser Leu Gln

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aaa tta aag gaa cat cta gtc ttc aca gta tgt tta tca tat cag tac 2240

Lys Leu Lys Glu His Leu Val Phe Thr Val Cys Leu Ser Tyr Gln Tyr

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685

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tca gga ttg gaa gat act gta gag gac aag cag gaa gtg aat gtt ggg 2288

Ser Gly Leu Glu Asp Thr Val Glu Asp Lys Gln Glu Val Asn Val Gly

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aaa cct ctc att gct aaa tta gac atg cat cga ggt ttg gga agg aag 2336

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act tgc ttt caa act tgt ctt atg tct aat ggt cct tac cag agt tct 2384

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Ala Ala Thr Ser Gly Gly Ala Gly His Tyr His Ser Leu Gln Asp Pro

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Phe His Gly Val Tyr His Ser His Pro Gly Asn Pro Ser Asn Val Thr

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Pro Ala Asp Ser Cys His Cys Ser Arg Thr Pro Asp Ala Phe Ile Ser

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795

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gta gag aca act gat gaa ata cca ttt agt ttc tct gac agg ctc aga 2624

Val Glu Thr Thr Asp Glu Ile Pro Phe Ser Phe Ser Asp Arg Leu Arg

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ctgtgaaata gtactgcact tacataaagt gagacattgt gaaaaggcaa atttgtatat 2736

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Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu Phe Asp

50 55 60

Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln Phe Lys

65 70 75 80

Asn Pro Leu Ile Met Leu Leu Leu Ala Ser Ala Val Ile Ser Val Leu

85 90 95

Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile Leu Ile

100 105 110

Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys Ser Leu

115 120 125

Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val Arg Glu

130

135

140

Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly Asp Thr

145

150

155

160

Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg Leu Phe

165

170

175

Glu Ala Val Asp Leu Ser Ile Asp Glu Ser Ser Leu Thr Gly Glu Thr

180

185

190

Thr Pro Cys Ser Lys Val Thr Ala Pro Gln Pro Ala Ala Thr Asn Gly

195

200

205

Asp Leu Ala Ser Arg Ser Asn Ile Ala Phe Met Gly Thr Leu Val Arg

210

215

220

Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn Ser Glu

225

230

235

240

Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro Lys Thr

245

250

255

Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser Phe Tyr

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Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu Leu Gly

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Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala Val Ala
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Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu Ala Leu
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Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys Leu Pro
325 330 335

Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp Lys Thr
340 345 350

Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe Thr Ser
355 360 365

Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln Phe Gly
370 375 380

Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn Pro Ala
385 390 395 400

Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala Val Ile
405 410 415

Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu Ile Ala
420 425 430

Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr Ile Arg
435 440 445

Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala Val Lys
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Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe Met Lys
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Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln Ser Lys
485 490 495

Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr Gln Gln
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Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala Leu Ala
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Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val Gly Ile
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Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr Leu Ile
545 550 555 560

Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln Glu Thr
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Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala Ala Asp

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Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile Leu Trp

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735

Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly Val Glu

740

745

750

Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp Lys Asp

755

760

765

Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser Ser Ile

770

775

780

Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu Arg Asp

785

790

795

800

Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys Phe Val

805

810

815

Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr Lys Ser

820

825

830

Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr Ala Val

835

840

845

Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro Pro Leu

850

855

860

Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu Leu Phe

865

870

875

880

Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile Ile Lys

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Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser Ser Thr

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Ser Ser Ser Phe Leu Glu Val

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ccagtgtggc cgtggctgac actaaagact ttgtagccat caaccgagt gcagtttcga 420

tgga aa atg aag gtt gca cgt ttt caa aaa ata cct aat ggt gaa aat 468

Met Lys Val Ala Arg Phe Gln Lys Ile Pro Asn Gly Glu Asn

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gag aca atg att cct gta ttg aca tca aaa aaa gca agt gaa tta cca 516

Glu Thr Met Ile Pro Val Leu Thr Ser Lys Lys Ala Ser Glu Leu Pro

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gtc agt gaa gtt gca agc att ctc caa gct gat ctt cag aat ggt cta 564

Val Ser Glu Val Ala Ser Ile Leu Gln Ala Asp Leu Gln Asn Gly Leu

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Asn Lys Cys Glu Val Ser His Arg Arg Ala Phe His Gly Trp Asn Glu

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Phe Asp Ile Ser Glu Asp Glu Pro Leu Trp Lys Lys Tyr Ile Ser Gln

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Val Leu Met His Gln Phe Asp Asp Ala Val Ser Ile Thr Val Ala Ile

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ctt atc gtt gtt aca gtt gcc ttt gtt cag gaa tat cgt tca gaa aaa 804

Leu Ile Val Val Thr Val Ala Phe Val Gln Glu Tyr Arg Ser Glu Lys

115 120 125

tct ctt gaa gaa ttg agt aaa ctt gtg cca cca gaa tgc cat tgt gtg 852

Ser Leu Glu Glu Leu Ser Lys Leu Val Pro Pro Glu Cys His Cys Val

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cgt gaa gga aaa ttg gag cat aca ctt gcc cga gac ttg gtt cca ggt 900

Arg Glu Gly Lys Leu Glu His Thr Leu Ala Arg Asp Leu Val Pro Gly

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Asp Thr Val Cys Leu Ser Val Gly Asp Arg Val Pro Ala Asp Leu Arg

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175 180 185 190

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195 200 205

aat gga gat ctt gca tcg aga agt aac att gcc ttt atg gga aca ctg 1092

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Val Arg Cys Gly Lys Ala Lys Gly Val Val Ile Gly Thr Gly Glu Asn

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tct gaa ttt ggg gag gtt ttt aaa atg atg caa gca gaa gag gca cca 1188

Ser Glu Phe Gly Glu Val Phe Lys Met Met Gln Ala Glu Glu Ala Pro

240

245

250

aaa acc cct ctg cag aag agc atg gac ctc tta gga aaa caa ctt tcc 1236

Lys Thr Pro Leu Gln Lys Ser Met Asp Leu Leu Gly Lys Gln Leu Ser

255

260

265

270

ttt tac tcc ttt ggt ata ata gga atc atc atg ttg gtt ggc tgg tta 1284

Phe Tyr Ser Phe Gly Ile Ile Gly Ile Ile Met Leu Val Gly Trp Leu

275

280

285

ctg gga aaa gat atc ctg gaa atg ttt act att agt gta agt ttg gct 1332

Leu Gly Lys Asp Ile Leu Glu Met Phe Thr Ile Ser Val Ser Leu Ala

290

295

300

gta gca gca att cct gaa ggt ctc ccc att gtg gtc aca gtg acg cta 1380

Val Ala Ala Ile Pro Glu Gly Leu Pro Ile Val Val Thr Val Thr Leu

305

310

315

gct ctt ggt gtt atg aga atg gtg aag aaa agg gcc att gtg aaa aag 1428

Ala Leu Gly Val Met Arg Met Val Lys Lys Arg Ala Ile Val Lys Lys

320

325

330

ctg cct att gtt gaa act ctg ggc tgc tgt aat gtg att tgt tca gat 1476

Leu Pro Ile Val Glu Thr Leu Gly Cys Cys Asn Val Ile Cys Ser Asp

335

340

345

350

aaa act gga aca ctg acg aag aat gaa atg act gtt act cac ata ttt 1524

Lys Thr Gly Thr Leu Thr Lys Asn Glu Met Thr Val Thr His Ile Phe

355

360

365

act tca gat ggt ctg cat gct gag gtt act gga gtt ggc tat aat caa 1572

Thr Ser Asp Gly Leu His Ala Glu Val Thr Gly Val Gly Tyr Asn Gln

370

375

380

ttt ggg gaa gtg att gtt gat ggt gat gtt gtt cat gga ttc tat aac 1620

Phe Gly Glu Val Ile Val Asp Gly Asp Val Val His Gly Phe Tyr Asn

385

390

395

cca gct gtt agc aga att gtt gag gcg ggc tgt gtg tgc aat gat gct 1668

Pro Ala Val Ser Arg Ile Val Glu Ala Gly Cys Val Cys Asn Asp Ala

400

405

410

gta att aga aac aat act cta atg ggg aag cca aca gaa ggg gcc tta 1716

Val Ile Arg Asn Asn Thr Leu Met Gly Lys Pro Thr Glu Gly Ala Leu

415

420

425

430

att gct ctt gca atg aag atg ggt ctt gat gga ctt caa caa gac tac 1764

Ile Ala Leu Ala Met Lys Met Gly Leu Asp Gly Leu Gln Gln Asp Tyr

435

440

445

atc aga aaa gct gaa tac cct ttt agc tct gag caa aag tgg atg gct 1812

Ile Arg Lys Ala Glu Tyr Pro Phe Ser Ser Glu Gln Lys Trp Met Ala

450

455

460

gtt aag tgt gta cac cga aca cag cag gac aga cca gag att tgt ttt 1860
 Val Lys Cys Val His Arg Thr Gln Gln Asp Arg Pro Glu Ile Cys Phe
 465 470 475

atg aaa ggt gct tac gaa caa gta att aag tac tgt act aca tac cag 1908
 Met Lys Gly Ala Tyr Glu Gln Val Ile Lys Tyr Cys Thr Thr Tyr Gln
 480 485 490

agc aaa ggg cag acc ttg aca ctt act cag cag cag aga gat gtg tac 1956
 Ser Lys Gly Gln Thr Leu Thr Leu Thr Gln Gln Gln Arg Asp Val Tyr
 495 500 505 510

caa caa gag aag gca cgc atg ggc tca gcg gga ctc aga gtt ctt gct 2004
 Gln Gln Glu Lys Ala Arg Met Gly Ser Ala Gly Leu Arg Val Leu Ala
 515 520 525

ttg gct tct ggt cct gaa ctg gga cag ctg aca ttt ctt ggc ttg gtg 2052
 Leu Ala Ser Gly Pro Glu Leu Gly Gln Leu Thr Phe Leu Gly Leu Val
 530 535 540

gga atc att gat cca cct aga act ggt gtg aaa gaa gct gtt aca aca 2100
 Gly Ile Ile Asp Pro Pro Arg Thr Gly Val Lys Glu Ala Val Thr Thr
 545 550 555

ctc att gcc tca gga gta tca ata aaa atg att act gga gat tca cag 2148
 Leu Ile Ala Ser Gly Val Ser Ile Lys Met Ile Thr Gly Asp Ser Gln
 560 565 570

gag act gca gtt gca atc gcc agt cgt ctg gga ttg tat tcc aaa act 2196

Glu Thr Ala Val Ala Ile Ala Ser Arg Leu Gly Leu Tyr Ser Lys Thr
575 580 585 590

tcc cag tca gtc tca gga gaa gaa ata gat gca atg gat gtt cag cag 2244
Ser Gln Ser Val Ser Gly Glu Glu Ile Asp Ala Met Asp Val Gln Gln
595 600 605

ctt tca caa ata gta cca aag gtt gca gta ttt tac aga gct agc cca 2292
Leu Ser Gln Ile Val Pro Lys Val Ala Val Phe Tyr Arg Ala Ser Pro
610 615 620

agg cac aag atg aaa att att aag tcg cta cag aag aac ggt tca gtt 2340
Arg His Lys Met Lys Ile Ile Lys Ser Leu Gln Lys Asn Gly Ser Val
625 630 635

gta gcc atg aca gga gat gga gta aat gat gca gtt gct ctg aag gct 2388
Val Ala Met Thr Gly Asp Gly Val Asn Asp Ala Val Ala Leu Lys Ala
640 645 650

gca gac att gga gtt gcg atg ggc cag act ggt aca gat gtt tgc aaa 2436
Ala Asp Ile Gly Val Ala Met Gly Gln Thr Gly Thr Asp Val Cys Lys
655 660 665 670

gag gca gca gac atg atc cta gtg gat gat gat ttt caa acc ata atg 2484
Glu Ala Ala Asp Met Ile Leu Val Asp Asp Asp Phe Gln Thr Ile Met
675 680 685

tct gca atc gaa gag ggt aaa ggg att tat aat aac att aaa aat ttc 2532
Ser Ala Ile Glu Glu Gly Lys Gly Ile Tyr Asn Asn Ile Lys Asn Phe

690

695

700

g t t a g a t t c c a g c t g a g c a c g a g t a t a g c a g c a t t a a c t t t a a t c t c a 2580

Val Arg Phe Gln Leu Ser Thr Ser Ile Ala Ala Leu Thr Leu Ile Ser

705

710

715

t t g g c t a c a t t a a t g a a c t t t c c t a a t c c t c t c a a t g c c a t g c a g a t t 2628

Leu Ala Thr Leu Met Asn Phe Pro Asn Pro Leu Asn Ala Met Gln Ile

720

725

730

t t g t g g a t c a a t a t t a t t a t g g a t g g a c c c c c a g c t c a g a g c c t t g g a 2676

Leu Trp Ile Asn Ile Ile Met Asp Gly Pro Pro Ala Gln Ser Leu Gly

735

740

745

750

g t a g a a c c a g t g g a t a a a g a t g t c a t t c g t a a a c c t c c t c g c a a c t g g 2724

Val Glu Pro Val Asp Lys Asp Val Ile Arg Lys Pro Pro Arg Asn Trp

755

760

765

a a a g a c a g c a t t t t g a c t a a a a a c t t g a t a c t t a a a a t a c t t g t t c a 2772

Lys Asp Ser Ile Leu Thr Lys Asn Leu Ile Leu Lys Ile Leu Val Ser

770

775

780

t c a a t a a t c a t t g t t t g t g g g a c t t t g t t t g t c t t c t g g c g t g a g c t a 2820

Ser Ile Ile Ile Val Cys Gly Thr Leu Phe Val Phe Trp Arg Glu Leu

785

790

795

c g a g a c a a t g t g a t t a c a c c t c g a g a c a c a a c a t g a c c t t c a c a t g c 2868

Arg Asp Asn Val Ile Thr Pro Arg Asp Thr Thr Met Thr Phe Thr Cys

800

805

810

ttt gtg ttt ttt gac atg ttc aat gca cta agt tcc aga tcc cag acc 2916

Phe Val Phe Phe Asp Met Phe Asn Ala Leu Ser Ser Arg Ser Gln Thr

815

820

825

830

aag tct gtg ttt gag att gga ctc tgc agt aat aga atg ttt tgc tat 2964

Lys Ser Val Phe Glu Ile Gly Leu Cys Ser Asn Arg Met Phe Cys Tyr

835

840

845

gca gtt ctt gga tcc atc atg gga caa tta cta gtt att tac ttt cct 3012

Ala Val Leu Gly Ser Ile Met Gly Gln Leu Leu Val Ile Tyr Phe Pro

850

855

860

ccg ctt cag aag gtt ttt cag act gag agc cta agc ata ctg gat ctg 3060

Pro Leu Gln Lys Val Phe Gln Thr Glu Ser Leu Ser Ile Leu Asp Leu

865

870

875

ttg ttt ctt ttg ggt ctc acc tca tca gtg tgc ata gtg gca gaa att 3108

Leu Phe Leu Leu Gly Leu Thr Ser Ser Val Cys Ile Val Ala Glu Ile

880

885

890

ata aag aag gtt gaa agg agc agg gaa aag atc cag aag cat gtt agt 3156

Ile Lys Lys Val Glu Arg Ser Arg Glu Lys Ile Gln Lys His Val Ser

895

900

905

910

tcg aca tca tca tct ttt ctt gaa gta tgatgcatat tgcattattt 3203

Ser Thr Ser Ser Ser Phe Leu Glu Val

915

tatttgcaaa ctaggaattg cagtctgagg atcatttaga agggcaagtt caagaggata 3263

tgaagatttg agaacttttt aactattcat tgactaaaaa tgaacattaa tgttaaagac 3323

ttaagacttt aacctgctgg cagtcccaaa tgaaattatg caactttgat atcatattcc 3383

ttgatttaaa ttggcttttg tgattgagtg aaactttata aagcatatgg tcagttattt 3443

aattaaaaag gcaaaacctg aaccaccttc tgcacttaaa gaagtctaac agtacaaata 3503

cactatctat cttagataga tatatTTTTT tttatTTTTa aatattgtac tatttatggt 3563

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<211> 382

<212> PRT

<213> Homo sapiens

<400> 135

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20

25

30

Arg Val Glu Met Glu Asp Ala His Thr Ala Val Ile Gly Leu Pro Ser

35

40

45

Gly Leu Glu Ser Trp Ser Phe Phe Ala Val Tyr Asp Gly His Ala Gly

50

55

60

Ser Gln Val Ala Lys Tyr Cys Cys Glu His Leu Leu Asp His Ile Thr

65

70

75

80

Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly Ala Pro Ser Val Glu Asn

85

90

95

Val Lys Asn Gly Ile Arg Thr Gly Phe Leu Glu Ile Asp Glu His Met

100

105

110

Arg Val Met Ser Glu Lys Lys His Gly Ala Asp Arg Ser Gly Ser Thr

115

120

125

Ala Val Gly Val Leu Ile Ser Pro Gln His Thr Tyr Phe Ile Asn Cys

130

135

140

Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn Arg Lys Val His Phe Phe

145

150

155

160

Thr Gln Asp His Lys Pro Ser Asn Pro Leu Glu Lys Glu Arg Ile Gln

165

170

175

Asn Ala Gly Gly Ser Val Met Ile Gln Arg Val Asn Gly Ser Leu Ala

180

185

190

Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr Lys Cys Val His Gly Lys

195

200

205

Gly Pro Thr Glu Gln Leu Val Ser Pro Glu Pro Glu Val His Asp Ile

210

215

220

Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile Ile Leu Ala Cys Asp Gly

225

230

235

240

Ile Trp Asp Val Met Gly Asn Glu Glu Leu Cys Asp Phe Val Arg Ser

245

250

255

Arg Leu Glu Val Thr Asp Asp Leu Glu Lys Val Cys Asn Glu Val Val

260

265

270

Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp Asn Met Ser Val Ile Leu

275

280

285

Ile Cys Phe Pro Asn Ala Pro Lys Val Ser Pro Glu Ala Val Lys Lys

290

295

300

Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys Arg Val Glu Glu Ile Ile

305

310

315

320

Lys Lys Gln Gly Glu Gly Val Pro Asp Leu Val His Val Met Arg Thr

325

330

335

Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro Pro Gly Gly Glu Leu Ala

340

345

350

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365

Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr Asp Asp Met Trp

370

375

380

<210> 136

<211> 2467

<212> DNA

<213> Homo sapiens

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<222> (444)..(1589)

<400> 136

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cgggtcctca ggcggtctgtt gctccggaac gggtaggttg ggaggggggg gtgggggggac 120

tctagacagc tgaggcgcga aagcgatgag tctcggctc ttctcctcc ttctccggga 180

cccgtctctt gcctccctct ccaacgccc gatgatctga gccgcgaggg cgcgcacagc 240

cgggggcccg gacgcagccc ggctcctccc ctctccgcc ccttccccag cctgacctgg 300

cccgcgctg cagcgggtgac cctcccccg gctgccgccg tcgccgccgc ggtgaccccc 360

tccccggctg ccgccgccgc cgcctcggcc gaccagggac ctgcccgcct gcggctgctc 420

cggacctaga ggatcaagac ata atg gga gca ttt tta gac aag cca aag atg 473

Met Gly Ala Phe Leu Asp Lys Pro Lys Met

1 5 10

gaa aag cat aat gcc cag ggg cag ggt aat ggg ttg cga tat ggg cta 521

Glu Lys His Asn Ala Gln Gly Gln Gly Asn Gly Leu Arg Tyr Gly Leu

15 20 25

agc agc atg caa ggc tgg cgt gtt gaa atg gag gat gca cat acg gct 569

Ser Ser Met Gln Gly Trp Arg Val Glu Met Glu Asp Ala His Thr Ala

30 35 40

gtg atc ggt ttg cca agt gga ctt gaa tcg tgg tca ttc ttt gct gtg 617

Val Ile Gly Leu Pro Ser Gly Leu Glu Ser Trp Ser Phe Phe Ala Val

45 50 55

tat gat ggg cat gct ggt tct cag gtt gcc aaa tac tgc tgt gag cat 665

Tyr Asp Gly His Ala Gly Ser Gln Val Ala Lys Tyr Cys Cys Glu His

60 65 70

ttg tta gat cac atc acc aat aac cag gat ttt aaa ggg tct gca gga 713

Leu Leu Asp His Ile Thr Asn Asn Gln Asp Phe Lys Gly Ser Ala Gly

75 80 85 90

gca cct tct gtg gaa aat gta aag aat gga atc aga aca ggt ttt ctg 761

Ala Pro Ser Val Glu Asn Val Lys Asn Gly Ile Arg Thr Gly Phe Leu

95 100 105

gag att gat gaa cac atg aga gtt atg tca gag aag aaa cat ggt gca 809

Glu Ile Asp Glu His Met Arg Val Met Ser Glu Lys Lys His Gly Ala

110

115

120

gat aga agt ggg tca aca gct gta ggt gtc tta att tct ccc caa cat 857

Asp Arg Ser Gly Ser Thr Ala Val Gly Val Leu Ile Ser Pro Gln His

125

130

135

act tat ttc att aac tgt gga gac tca aga ggt tta ctt tgt agg aac 905

Thr Tyr Phe Ile Asn Cys Gly Asp Ser Arg Gly Leu Leu Cys Arg Asn

140

145

150

agg aaa gtt cat ttc ttc aca caa gat cac aaa cca agt aat ccg ctg 953

Arg Lys Val His Phe Phe Thr Gln Asp His Lys Pro Ser Asn Pro Leu

155

160

165

170

gag aaa gaa cga att cag aat gca ggt ggc tct gta atg att cag cgt 1001

Glu Lys Glu Arg Ile Gln Asn Ala Gly Gly Ser Val Met Ile Gln Arg

175

180

185

gtg aat ggc tct ctg gct gta tcg agg gcc ctt ggg gat ttt gat tac 1049

Val Asn Gly Ser Leu Ala Val Ser Arg Ala Leu Gly Asp Phe Asp Tyr

190

195

200

aaa tgt gtc cat gga aaa ggt cct act gag cag ctt gtc tca cca gag 1097

Lys Cys Val His Gly Lys Gly Pro Thr Glu Gln Leu Val Ser Pro Glu

205

210

215

cct gaa gtc cat gat att gaa aga tct gaa gaa gat gat cag ttc att 1145

Pro Glu Val His Asp Ile Glu Arg Ser Glu Glu Asp Asp Gln Phe Ile

220

225

230

atc ctt gca tgt gat ggt atc tgg gat gtt atg gga aat gaa gag ctc 1193

Ile Leu Ala Cys Asp Gly Ile Trp Asp Val Met Gly Asn Glu Glu Leu

235

240

245

250

tgt gat ttt gta aga tcc aga ctt gaa gtc act gat gac ctt gag aaa 1241

Cys Asp Phe Val Arg Ser Arg Leu Glu Val Thr Asp Asp Leu Glu Lys

255

260

265

gtt tgc aat gaa gta gtc gac acc tgt ttg tat aag gga agt cga gac 1289

Val Cys Asn Glu Val Val Asp Thr Cys Leu Tyr Lys Gly Ser Arg Asp

270

275

280

aac atg agt gtg att ttg atc tgt ttt cca aat gca ccc aaa gta tcg 1337

Asn Met Ser Val Ile Leu Ile Cys Phe Pro Asn Ala Pro Lys Val Ser

285

290

295

cca gaa gca gtg aag aag gag gca gag ttg gac aag tac ctg gaa tgc 1385

Pro Glu Ala Val Lys Lys Glu Ala Glu Leu Asp Lys Tyr Leu Glu Cys

300

305

310

aga gta gaa gaa atc ata aag aag cag ggg gaa ggc gtc ccc gac tta 1433

Arg Val Glu Glu Ile Ile Lys Lys Gln Gly Glu Gly Val Pro Asp Leu

315

320

325

330

gtc cat gtg atg cgc aca tta gcg agt gag aac atc ccc agc ctc cca 1481

Val His Val Met Arg Thr Leu Ala Ser Glu Asn Ile Pro Ser Leu Pro

335

340

345

cca ggg ggt gaa ttg gca agc aag agg aat gtt att gaa gcc gtt tac 1529

Pro Gly Gly Glu Leu Ala Ser Lys Arg Asn Val Ile Glu Ala Val Tyr

350

355

360

aat aga ctg aat cct tac aaa aat gac gac act gac tct aca tca aca 1577

Asn Arg Leu Asn Pro Tyr Lys Asn Asp Asp Thr Asp Ser Thr Ser Thr

365

370

375

gat gat atg tgg taaaactgct catctagcca tggagtttac cttcacctcc 1629

Asp Asp Met Trp

380

aaaggagagt acagctcaac tttgttgaaa cttttaacat ccatacctcaa ctttaaggaa 1689

ggggatatga catgggtgag aatgattaca tcagagaact tcagcagtagc aacagctagc 1749

ccagaactga tttttttttt ttttttgtaa atttgagact tatgtaagcg tgatttcaaa 1809

ccataattcg tgttgtaaatt cagactccag caatttttgt tgtatgattt tgtttttttg 1869

taaagtgtaa ttgtccttgt acaaaatgct catatttaatt tatgaactgc tttaaatacac 1929

tatcaaagtt acaagaaatg tttggcttat tgtgtgatgc aacagatatata tagccctttc 1989

aagtcatgtt gtgttttgac ttgggggttg aacagggaga gcagcagcca tgtagctac 2049

acgctcaaat gtgcagatga ttatggaaaa taacctcaaa atcttacaaa gctgaacatc 2109

caaggagtta ttgaaaacta tcttaaagt tcttggtagg ggagttggca ttgttgataa 2169

agccagtcctc ttcatttaac tgtctttcag gatgttcctt cgttgtttcc atgagtattg 2229

caggtataaa tacagtgtat tcataagaat ctcaatcttg gggctaaatg ccttgtttct 2289

ttgcacctct tttcaagtc ttacatttaa ttactaattg ataagcagca gcttcctaca 2349

tatagtagga aactgccaca tttttgctat catgattggc tgggcctgct gctgttccta 2409

gtaagatatt ctgaattcca ttttatcaat aaagcttgat ttaacaaaca agaaactt 2467

<210> 137

<211> 358

<212> PRT

<213> Homo sapiens

<400> 137

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Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp

20 25 30

Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu

35 40 45

Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val
50 55 60

Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg
65 70 75 80

Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn
85 90 95

Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser
100 105 110

Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser
115 120 125

Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met
130 135 140

Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala
145 150 155 160

Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser
165 170 175

Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr
180 185 190

Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln

195

200

205

Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln

210

215

220

Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro

225

230

235

240

Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln

245

250

255

Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln

260

265

270

Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr

275

280

285

Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln

290

295

300

Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly

305

310

315

320

Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro

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340

345

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Pro Gly Pro Gly Tyr Arg

355

<210> 138

<211> 1519

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (11)..(1084)

<400> 138

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gat gaa gta aca ata aag tat aaa gat gaa gat gga gat ctt ata aca 97

Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp Leu Ile Thr

15

20

25

att ttt gat agt tct gac ctt tcc ttt gca att cag tgc agt agg ata 145

Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys Ser Arg Ile

30

35

40

45

ctg aaa ctg aca tta ttt gtt aat ggc cag cca aga ccc ctt gaa tca 193

Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro Leu Glu Ser

50

55

60

agt cag gtg aaa tat ctc cgt cga gaa ctg ata gaa ctt cga aat aaa 241

Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu Arg Asn Lys

65

70

75

gtg aat cgt tta ttg gat agc ttg gaa cca cct gga gaa cca gga cct 289

Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu Pro Gly Pro

80

85

90

tcc acc aat att cct gaa aat gat act gtg gat ggt agg gaa gaa aag 337

Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg Glu Glu Lys

95

100

105

tct gct tct gat tct tct gga aaa cag tct act cag gtt atg gca gca 385

Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val Met Ala Ala

110

115

120

125

agt atg tct gct ttt gat cct tta aaa aac caa gat gaa atc aat aaa 433

Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu Ile Asn Lys

130

135

140

aat gtt atg tca gcg ttt ggc tta aca gat gat cag gtt tca ggg cca 481

Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val Ser Gly Pro

145

150

155

ccc agt gct cct gca gaa gat cgt tca gga aca ccc gac agc att gct 529

Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp Ser Ile Ala

160

165

170

tcc tcc tcc tca gca gct cac cca cca ggc gtt cag cca cag cag cca 577
 Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro Gln Gln Pro
 175 180 185

cca tat aca gga gct cag act caa gca ggt cag atg tac caa cag tac 625
 Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr Gln Gln Tyr
 190 195 200 205

cag caa cag gcc ggc tat ggt gca cag cag ccg cag gct cca cct cag 673
 Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala Pro Pro Gln
 210 215 220

cag cct caa cag tat ggt att cag tat tca gca agc tat agt cag cag 721
 Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr Ser Gln Gln
 225 230 235

act gga ccc caa caa cct cag cag ttc cag gga tat ggc cag caa cca 769
 Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly Gln Gln Pro
 240 245 250

act tcc cag gca cca gct cct gcc ttt tct ggt cag cct caa caa ctg 817
 Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro Gln Gln Leu
 255 260 265

cct gct cag ccg cca cag cag tac cag gcg agc aat tat cct gca caa 865
 Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr Pro Ala Gln
 270 275 280 285

act tac act gcc caa act tct cag cct act aat tat act gtg gct cct 913

Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr Val Ala Pro
 290 295 300

gcc tct caa cct gga atg gct cca agc caa cct ggg gcc tat caa cca 961
 Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala Tyr Gln Pro
 305 310 315

aga cca ggt ttt act tca ctt cct gga agt acc atg acc cct cct cca 1009
 Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr Pro Pro Pro
 320 325 330

agt ggg cct aat cct tat gcg cgt aac cgt cct ccc ttt ggt cag ggc 1057
 Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe Gly Gln Gly
 335 340 345

tat acc caa cct gga cct ggt tat cga taaggaggct cctctacacc 1104
 Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
 350 355

aattaatgta gctgctagct attggcctcc caaaagactc cagtactatt ttaatttgta 1164

ttgaagaagt tcagaaattt aaaagcagag cattttttat gatattcattg ttggtgttaa 1224

ttgaaagtat aatttgctgg aacacaaaga ccaaaatgaa agttttttcc tcctgctta 1284

aaaatgtagc agcttcttag ttactttgga acactactct tacatgtata aagtattga 1344

cttgactttc tagcttcct tgtccggagg atattaaaat gctagggtga ggtttagcca 1404

tcttacttgg ctttttacta ttaacatgat gtactaaagt agagcccttt gagaatacaa 1464

gatattatgt ataaaatgta acactgatga taggttaata aagatgattg aatcc 1519

<210> 139

<211> 396

<212> PRT

<213> Homo sapiens

<400> 139

Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu Ile Val Lys Ala Gln

1 5 10 15

Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His Asn Glu Asp Ile Thr

20 25 30

Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val Phe Arg Gly Lys Leu

35 40 45

Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys Asp Glu Asp Gly Asp

50 55 60

Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser Phe Ala Ile Gln Cys

65 70 75 80

Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn Gly Gln Pro Arg Pro

85 90 95

Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg Glu Leu Ile Glu Leu
100 105 110

Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu Glu Pro Pro Gly Glu
115 120 125

Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp Thr Val Asp Gly Arg
130 135 140

Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys Gln Ser Thr Gln Val
145 150 155 160

Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu Lys Asn Gln Asp Glu
165 170 175

Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu Thr Asp Asp Gln Val
180 185 190

Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg Ser Gly Thr Pro Asp
195 200 205

Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro Pro Gly Val Gln Pro
210 215 220

Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln Ala Gly Gln Met Tyr
225 230 235 240

Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala Gln Gln Pro Gln Ala
245 250 255

Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln Tyr Ser Ala Ser Tyr
260 265 270

Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln Phe Gln Gly Tyr Gly
275 280 285

Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala Phe Ser Gly Gln Pro
290 295 300

Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr Gln Ala Ser Asn Tyr
305 310 315 320

Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln Pro Thr Asn Tyr Thr
325 330 335

Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro Ser Gln Pro Gly Ala
340 345 350

Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro Gly Ser Thr Met Thr
355 360 365

Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg Asn Arg Pro Pro Phe
370 375 380

Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr Arg
385 390 395

<210> 140
 <211> 1641
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (19)..(1206)

<400> 140

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aacatcctgg agtccacc atg aac gga cag ttg gat cta agt ggg aag cta   51
      Met Asn Gly Gln Leu Asp Leu Ser Gly Lys Leu
                1             5             10

atc gtc aaa gct caa ctt ggg gag gat att cgg cga att cct att cat   99
Ile Val Lys Ala Gln Leu Gly Glu Asp Ile Arg Arg Ile Pro Ile His
          15             20             25

aat gaa gat att act tat gat gaa tta gtg cta atg atg caa cga gtt   147
Asn Glu Asp Ile Thr Tyr Asp Glu Leu Val Leu Met Met Gln Arg Val
          30             35             40

ttc aga gga aaa ctt ctg agt aat gat gaa gta aca ata aag tat aaa   195
Phe Arg Gly Lys Leu Leu Ser Asn Asp Glu Val Thr Ile Lys Tyr Lys
          45             50             55

gat gaa gat gga gat ctt ata aca att ttt gat agt tct gac ctt tcc   243
Asp Glu Asp Gly Asp Leu Ile Thr Ile Phe Asp Ser Ser Asp Leu Ser
          60             65             70             75

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ttt gca att cag tgc agt agg ata ctg aaa ctg aca tta ttt gtt aat 291

Phe Ala Ile Gln Cys Ser Arg Ile Leu Lys Leu Thr Leu Phe Val Asn

80

85

90

ggc cag cca aga ccc ctt gaa tca agt cag gtg aaa tat ctc cgt cga 339

Gly Gln Pro Arg Pro Leu Glu Ser Ser Gln Val Lys Tyr Leu Arg Arg

95

100

105

gaa ctg ata gaa ctt cga aat aaa gtg aat cgt tta ttg gat agc ttg 387

Glu Leu Ile Glu Leu Arg Asn Lys Val Asn Arg Leu Leu Asp Ser Leu

110

115

120

gaa cca cct gga gaa cca gga cct tcc acc aat att cct gaa aat gat 435

Glu Pro Pro Gly Glu Pro Gly Pro Ser Thr Asn Ile Pro Glu Asn Asp

125

130

135

act gtg gat ggt agg gaa gaa aag tct gct tct gat tct tct gga aaa 483

Thr Val Asp Gly Arg Glu Glu Lys Ser Ala Ser Asp Ser Ser Gly Lys

140

145

150

155

cag tct act cag gtt atg gca gca agt atg tct gct ttt gat cct tta 531

Gln Ser Thr Gln Val Met Ala Ala Ser Met Ser Ala Phe Asp Pro Leu

160

165

170

aaa aac caa gat gaa atc aat aaa aat gtt atg tca gcg ttt ggc tta 579

Lys Asn Gln Asp Glu Ile Asn Lys Asn Val Met Ser Ala Phe Gly Leu

175

180

185

aca gat gat cag gtt tca ggg cca ccc agt gct cct gca gaa gat cgt 627

Thr Asp Asp Gln Val Ser Gly Pro Pro Ser Ala Pro Ala Glu Asp Arg

190

195

200

tca gga aca ccc gac agc att gct tcc tcc tcc tca gca gct cac cca 675

Ser Gly Thr Pro Asp Ser Ile Ala Ser Ser Ser Ser Ala Ala His Pro

205

210

215

cca ggc gtt cag cca cag cag cca cca tat aca gga gct cag act caa 723

Pro Gly Val Gln Pro Gln Gln Pro Pro Tyr Thr Gly Ala Gln Thr Gln

220

225

230

235

gca ggt cag atg tac caa cag tac cag caa cag gcc ggc tat ggt gca 771

Ala Gly Gln Met Tyr Gln Gln Tyr Gln Gln Gln Ala Gly Tyr Gly Ala

240

245

250

cag cag ccg cag gct cca cct cag cag cct caa cag tat ggt att cag 819

Gln Gln Pro Gln Ala Pro Pro Gln Gln Pro Gln Gln Tyr Gly Ile Gln

255

260

265

tat tca gca agc tat agt cag cag act gga ccc caa caa cct cag cag 867

Tyr Ser Ala Ser Tyr Ser Gln Gln Thr Gly Pro Gln Gln Pro Gln Gln

270

275

280

ttc cag gga tat ggc cag caa cca act tcc cag gca cca gct cct gcc 915

Phe Gln Gly Tyr Gly Gln Gln Pro Thr Ser Gln Ala Pro Ala Pro Ala

285

290

295

ttt tct ggt cag cct caa caa ctg cct gct cag ccg cca cag cag tac 963

Phe Ser Gly Gln Pro Gln Gln Leu Pro Ala Gln Pro Pro Gln Gln Tyr
300 305 310 315

cag gcg agc aat tat cct gca caa act tac act gcc caa act tct cag 1011
Gln Ala Ser Asn Tyr Pro Ala Gln Thr Tyr Thr Ala Gln Thr Ser Gln
320 325 330

cct act aat tat act gtg gct cct gcc tct caa cct gga atg gct cca 1059
Pro Thr Asn Tyr Thr Val Ala Pro Ala Ser Gln Pro Gly Met Ala Pro
335 340 345

agc caa cct ggg gcc tat caa cca aga cca ggt ttt act tca ctt cct 1107
Ser Gln Pro Gly Ala Tyr Gln Pro Arg Pro Gly Phe Thr Ser Leu Pro
350 355 360

gga agt acc atg acc cct cct cca agt ggg cct aat cct tat gcg cgt 1155
Gly Ser Thr Met Thr Pro Pro Pro Ser Gly Pro Asn Pro Tyr Ala Arg
365 370 375

aac cgt cct ccc ttt ggt cag ggc tat acc caa cct gga cct ggt tat 1203
Asn Arg Pro Pro Phe Gly Gln Gly Tyr Thr Gln Pro Gly Pro Gly Tyr
380 385 390 395

cga taaggaggct cctctacacc aattaatgta gctgctagct attggcctcc 1256
Arg

caaaagactc cagtactatt ttaatttgta ttgaagaagt tcagaaattt aaaagcagag 1316

cattttttat gatattcattg ttggtgttaa ttgaaagtat aatttgctgg aacacaaaga 1376

ccaaaatgaa agttttttcc tccctgctta aaaatgtagc agcttcttag ttactttgga 1436

acactactct tacatgtata aagtgattga cttgactttc tagcttcctt tgtccggagg 1496

atattaaaat gctaggggtga ggttttagcca tcttacttgg ctttttacta ttaacatgat 1556

gtactaaagt agagcccttt gagaatacaa gatattatgt ataaaatgta acactgatga 1616

taggttaata aagatgattg aatcc 1641

<210> 141

<211> 323

<212> PRT

<213> Homo sapiens

<400> 141

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro Ala Val Pro

1 5 10 15

Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu Gln Ile Thr

20 25 30

Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe Ala Val Asn

35 40 45

Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro

50 55 60

Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg Gln Asn Gly
65 70 75 80

Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe Gln Lys Gly
85 90 95

Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp Phe Lys Val
100 105 110

Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg Val Pro Phe
115 120 125

His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln Leu Ser Tyr
130 135 140

Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro Ala Pro Ile
145 150 155 160

Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly Gln Met Phe
165 170 175

Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro Ala Tyr Pro
180 185 190

Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro Ser Lys Ser
195 200 205

Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg Phe His Ile

210

215

220

Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn Pro Arg Phe

225

230

235

240

Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn Ser Trp Gly

245

250

255

Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val Arg Gly Gln

260

265

270

Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu Lys Val Ala

275

280

285

Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu Arg Asn Leu

290

295

300

Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln Leu Thr His

305

310

315

320

Val Gln Thr

<210> 142

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (72)..(1040)

<400> 142

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gcggcggaga g atg gcc ttc agc ggt tcc cag gct ccc tac ctg agt cca 110

Met Ala Phe Ser Gly Ser Gln Ala Pro Tyr Leu Ser Pro

1

5

10

gct gtc ccc ttt tct ggg act att caa gga ggt ctc cag gac gga ctt 158

Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu Gln Asp Gly Leu

15

20

25

cag atc act gtc aat ggg acc gtt ctc agc tcc agt gga acc agg ttt 206

Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser Gly Thr Arg Phe

30

35

40

45

gct gtg aac ttt cag act ggc ttc agt gga aat gac att gcc ttc cac 254

Ala Val Asn Phe Gln Thr Gly Phe Ser Gly Asn Asp Ile Ala Phe His

50

55

60

ttc aac cct cgg ttt gaa gat gga ggg tac gtg gtg tgc aac acg agg 302

Phe Asn Pro Arg Phe Glu Asp Gly Gly Tyr Val Val Cys Asn Thr Arg

65

70

75

cag aac gga agc tgg ggg ccc gag gag agg aag aca cac atg cct ttc 350

Gln Asn Gly Ser Trp Gly Pro Glu Glu Arg Lys Thr His Met Pro Phe

80

85

90

cag aag ggg atg ccc ttt gac ctc tgc ttc ctg gtg cag agc tca gat 398

Gln Lys Gly Met Pro Phe Asp Leu Cys Phe Leu Val Gln Ser Ser Asp

95

100

105

ttc aag gtg atg gtg aac ggg atc ctc ttc gtg cag tac ttc cac cgc 446

Phe Lys Val Met Val Asn Gly Ile Leu Phe Val Gln Tyr Phe His Arg

110

115

120

125

gtg ccc ttc cac cgt gtg gac acc atc tcc gtc aat ggc tct gtg cag 494

Val Pro Phe His Arg Val Asp Thr Ile Ser Val Asn Gly Ser Val Gln

130

135

140

ctg tcc tac atc agc ttc cag cct ccc ggc gtg tgg cct gcc aac ccg 542

Leu Ser Tyr Ile Ser Phe Gln Pro Pro Gly Val Trp Pro Ala Asn Pro

145

150

155

gct ccc att acc cag aca gtc atc cac aca gtg cag agc gcc cct gga 590

Ala Pro Ile Thr Gln Thr Val Ile His Thr Val Gln Ser Ala Pro Gly

160

165

170

cag atg ttc tct act ccc gcc atc cca cct atg atg tac ccc cac ccc 638

Gln Met Phe Ser Thr Pro Ala Ile Pro Pro Met Met Tyr Pro His Pro

175

180

185

gcc tat ccg atg cct ttc atc acc acc att ctg gga ggg ctg tac cca 686

Ala Tyr Pro Met Pro Phe Ile Thr Thr Ile Leu Gly Gly Leu Tyr Pro

190

195

200

205

tcc aag tcc atc ctc ctg tca ggc act gtc ctg ccc agt gct cag agg 734
 Ser Lys Ser Ile Leu Leu Ser Gly Thr Val Leu Pro Ser Ala Gln Arg

210

215

220

ttc cac atc aac ctg tgc tct ggg aac cac atc gcc ttc cac ctg aac 782
 Phe His Ile Asn Leu Cys Ser Gly Asn His Ile Ala Phe His Leu Asn

225

230

235

ccc cgt ttt gat gag aat gct gtg gtc cgc aac acc cag atc gac aac 830
 Pro Arg Phe Asp Glu Asn Ala Val Val Arg Asn Thr Gln Ile Asp Asn

240

245

250

tcc tgg ggg tct gag gag cga agt ctg ccc cga aaa atg ccc ttc gtc 878
 Ser Trp Gly Ser Glu Glu Arg Ser Leu Pro Arg Lys Met Pro Phe Val

255

260

265

cgt ggc cag agc ttc tca gtg tgg atc ttg tgt gaa gct cac tgc ctc 926
 Arg Gly Gln Ser Phe Ser Val Trp Ile Leu Cys Glu Ala His Cys Leu

270

275

280

285

aag gtg gcc gtg gat ggt cag cac ctg ttt gaa tac tac cat cgc ctg 974
 Lys Val Ala Val Asp Gly Gln His Leu Phe Glu Tyr Tyr His Arg Leu

290

295

300

agg aac ctg ccc acc atc aac aga ctg gaa gtg ggg ggc gac atc cag 1022
 Arg Asn Leu Pro Thr Ile Asn Arg Leu Glu Val Gly Gly Asp Ile Gln

305

310

315

ctg acc cat gtg cag aca taggcggcctt cctggccctg gggccggggg 1070

Leu Thr His Val Gln Thr

320

ctgggggtgtg gggcagtcctg ggtcctctca tcatecccaac tteccaggcc cagcctttcc 1130

aaccctgcct gggatctggg ctttaatgca gaggccatgt ccttgtctgg tcctgcttct 1190

ggctacagcc accctggaac ggagaaggca gctgacgggg attgccttcc tcagccgcag 1250

cagcacctgg ggctccagct gctggaatcc taccatccca ggaggcaggc acagccaggg 1310

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gcagctccac cccagtcacca agccaccagc tgtctgctcc tgggtgggagg tggcctcctc 1430

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ccctcctgga aagcaggcct gatggcttcc cactggcctc caccacctga ccagagtgtt 1550

ctcttcagag gactggctcc ttteccagtg tccttaaaat aaagaaatga aaatgcttgt 1610

tggcac 1616

<210> 143

<211> 136

<212> PRT

<213> Homo sapiens

<400> 143

Met Ala Gly Ala Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile

1 5 10 15

Val Gly Gly Ile Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly

20 25 30

Gly Leu Ile Ala Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val

35 40 45

Lys Cys Val Asp Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val

50 55 60

Pro Trp Gly Pro Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala

65 70 75 80

Ile Pro Arg Glu Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile

85 90 95

Pro Leu Pro His Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His

100 105 110

Gly His Leu Ser Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe

115 120 125

Leu Gln Pro Leu Met His Cys Val

130 135

<210> 144
 <211> 1252
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (225)..(632)

<400> 144

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 ggcgcccttc gtcccgggtcc catcctcgcc gcgctccagc acctctgaag tttgcagcg 120
 cccagaaagg aggcgaggaa ggagggagtg tgtgagagga gggagcaaaa agctcacct 180
 aaaacattta tttcaaggag aaaagaaaaa gggggggcgc aaaa atg gct ggg gca 236

Met Ala Gly Ala

1

att ata gaa aac atg agc acc aag aag ctg tgc att gtt ggt ggg att 284
 Ile Ile Glu Asn Met Ser Thr Lys Lys Leu Cys Ile Val Gly Gly Ile
 5 10 15 20

ctg ctc gtg ttc caa atc atc gcc ttt ctg gtg gga ggc ttg att gct 332
 Leu Leu Val Phe Gln Ile Ile Ala Phe Leu Val Gly Gly Leu Ile Ala
 25 30 35

cca ggg ccc aca acg gca gtg tcc tac atg tgc gtg aaa tgt gtg gat 380
 Pro Gly Pro Thr Thr Ala Val Ser Tyr Met Ser Val Lys Cys Val Asp

40

45

50

gcc cgt aag aac cat cac aag aca aaa tgg ttc gtg cct tgg gga ccc 428
 Ala Arg Lys Asn His His Lys Thr Lys Trp Phe Val Pro Trp Gly Pro

55

60

65

aat cat tgt gac aag atc cga gac att gaa gag gca att cca agg gaa 476
 Asn His Cys Asp Lys Ile Arg Asp Ile Glu Glu Ala Ile Pro Arg Glu

70

75

80

att gaa gcc aat gac atc gtg ttt tct gtt cac att ccc ctc ccc cac 524
 Ile Glu Ala Asn Asp Ile Val Phe Ser Val His Ile Pro Leu Pro His

85

90

95

100

atg gct ctt agc tgt ggt ttc ttg gac cag cgg cat gga cat ttg tca 572
 Met Ala Leu Ser Cys Gly Phe Leu Asp Gln Arg His Gly His Leu Ser

105

110

115

gtt tgc ctt ctg acg gta gct ttt gga gga aga ttc ctg cag cca cta 620
 Val Cys Leu Leu Thr Val Ala Phe Gly Gly Arg Phe Leu Gln Pro Leu

120

125

130

atg cat tgt gta tgataacaaa aactctggta tgacacattt tctgtgatca 672
 Met His Cys Val

135

ttgttaatta gtgacatagt aacatctgta gcagctgggtt agtaaaccctc atgtgggggt 732

ggggtggggg tgtattcctt gggggatggt ttgggccgaa tggggagtgg aatatttgac 792

atttttcctg ttttaaattc taggatagat tttaacatcc ttgcggtcc cagtccaagg 852

taggctggtg tcatagtctt ctcactccta atccatgacc actgtttttt tcctatttat 912

atcaccaggt agcctactga gttaatattt aagttgtcaa tagataagtg tcctgtttt 972

gtggcataat ataactgaat ttcatgagaa gatttattcc accaggggta tttcagcttt 1032

gaaaccaaat ctgtgtatct aatactaacc aatctgttgg atgtgggttt taaaaaatgt 1092

ttgctaaact acccaagtaa gatttactgt attaaatggc cttcgggtct gaaaagcttt 1152

tttaacctct tgcttaaaat gcgttttatt ttgataagat acttcaaata gcctccaaaa 1212

gtgtagatcc aatcacttaa ataaacctgt atgtatatgc 1252

<210> 145

<211> 468

<212> PRT

<213> Homo sapiens

<400> 145

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser Cys Leu Gly Asp

1

5

10

15

Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg Gln Phe Gln Phe

20

25

30

Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe Lys Leu Asn Asn Gln

35

40

45

Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val Ser Leu Ala Tyr Arg

50

55

60

Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro

65

70

75

80

Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu

85

90

95

Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser

100

105

110

Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu

115

120

125

Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu

130

135

140

Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met

145

150

155

160

Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp

165

170

175

Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val
180 185 190

Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu
195 200 205

Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp
210 215 220

Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile
225 230 235 240

Phe Cys Gly Glu His Met Met Asp Gln His Glu Arg Asn His Ile Ala
245 250 255

Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu
260 265 270

Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe
275 280 285

Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe
290 295 300

Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys
305 310 315 320

Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser

325

330

335

Leu Pro Ala Met Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile

340

345

350

Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met

355

360

365

Thr Val Ile Phe Phe Ile Val Ser Gln Val Thr Glu Gly His Trp Lys

370

375

380

Trp Gly Gly Val Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile

385

390

395

400

Tyr Gly Met Trp Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala

405

410

415

Pro Ser His Lys Asn Tyr Gly Glu Asp Gln Ser Asn Gly Met Gln Leu

420

425

430

Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr

435

440

445

Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala

450

455

460

Ala Ser Gly Ile

465

<210> 146
 <211> 1943
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (379)..(1782)

<400> 146
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 tcacgcctt tctggtggga ggcttgattg ctccagggcc cacaacggca gtgtcctaca 360
 tgtcggtgaa atgtgtgg atg ccc gta aga acc atc aca aga caa aat ggt 411
 Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly
 1 5 10
 tcg tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag 459
 Ser Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys

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agg caa ttc caa ttc atg ctg ttt atc ctg cag ctg gac att gcc ttc 507

Arg Gln Phe Gln Phe Met Leu Phe Ile Leu Gln Leu Asp Ile Ala Phe

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35

40

aag cta aac aac caa atc aga gaa aat gca gaa gtc tcc atg gac gtt 555

Lys Leu Asn Asn Gln Ile Arg Glu Asn Ala Glu Val Ser Met Asp Val

45

50

55

tcc ctg gct tac cgt gat gac gcg ttt gct gag tgg act gaa atg gcc 603

Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr Glu Met Ala

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70

75

cat gaa aga gta cca cgg aaa ctc aaa tgc acc ttc aca tct ccc aag 651

His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr Ser Pro Lys

80

85

90

act cca gag cat gag ggc cgt tac tat gaa tgt gat gtc ctt cct ttc 699

Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val Leu Pro Phe

95

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atg gaa att ggg tct gtg gcc cat aag ttt tac ctt tta aac atc cgg 747

Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu Asn Ile Arg

110

115

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ctg cct gtg aat gag aag aag aaa atc aat gtg gga att ggg gag ata 795

Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile Gly Glu Ile

125

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aag gat atc cgg ttg gtg ggg atc cac caa aat gga ggc ttc acc aag 843

Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly Phe Thr Lys

140

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150

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gtg tgg ttt gcc atg aag acc ttc ctt acg ccc agc atc ttc atc att 891

Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile Phe Ile Ile

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Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg Pro Pro Val

175

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ctt ctg gaa aaa gtc atc ttt gcc ctt ggg att tcc atg acc ttt atc 987

Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met Thr Phe Ile

190

195

200

aat atc cca gtg gaa tgg ttt tcc atc ggg ttt gac tgg acc tgg atg 1035

Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp Thr Trp Met

205

210

215

ctg ctg ttt ggt gac atc cga cag ggc atc ttc tat gcg atg ctt ctg 1083

Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala Met Leu Leu

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225

230

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tcc ttc tgg atc atc ttc tgt ggc gag cac atg atg gat cag cac gag 1131

Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp Gln His Glu

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Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro Ile Ala Val

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ggc tcc ttc tgc ctc ttc ata ttt gac atg tgt gag aga ggg gta caa 1227

Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg Gly Val Gln

270

275

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ctc acg aat ccc ttc tac agt atc tgg act aca gac att gga aca gag 1275

Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile Gly Thr Glu

285

290

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ctg gcc atg gcc ttc atc atc gtg gct gga atc tgc ctc tgc ctc tac 1323

Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu Cys Leu Tyr

300

305

310

315

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Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg Asn Ile Ser

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335

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Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu Ile Thr Leu

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gcc tgc gct gcc atg act gtc atc ttc ttc atc gtt agt cag gta acg 1515

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365

370

375

gaa ggc cat tgg aaa tgg ggc ggc gtc aca gtc caa gtg aac agt gcc 1563

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380

385

390

395

ttt ttc aca ggc atc tat ggg atg tgg aat ctg tat gtc ttt gct ctg 1611

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400

405

410

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420

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aat gga atg caa ctc cca tgt aaa tcg agg gaa gat tgt gct ttg ttt 1707

Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys Ala Leu Phe

430

435

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gtt tcg gaa ctt tat caa gaa ttg ttc agc gct tcg aaa tat tcc ttc 1755

Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys Tyr Ser Phe

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atc aat gac aac gca gct tct ggt att tgagtcaaca aggcaacaca 1802

Ile Asn Asp Asn Ala Ala Ser Gly Ile

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acaaatacac tcatttagcc tttatctcaa aatgttaaata ataaggaaaa aagcgtcaac 1922

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<211> 460

<212> PRT

<213> Homo sapiens

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35 40 45

Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe Ala Glu Trp Thr

50 55 60

Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys Cys Thr Phe Thr

65 70 75 80

Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr Glu Cys Asp Val

85 90 95

Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys Phe Tyr Leu Leu
 100 105 110

Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile Asn Val Gly Ile
 115 120 125

Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His Gln Asn Gly Gly
 130 135 140

Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu Thr Pro Ser Ile
 145 150 155 160

Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr Met Met Ser Arg
 165 170 175

Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu Gly Ile Ser Met
 180 185 190

Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile Gly Phe Asp Trp
 195 200 205

Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly Ile Phe Tyr Ala
 210 215 220

Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu His Met Met Asp
 225 230 235 240

Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys Gln Val Gly Pro
 245 250 255

Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp Met Cys Glu Arg

260

265

270

Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp Thr Thr Asp Ile

275

280

285

Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala Gly Ile Cys Leu

290

295

300

Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe Gln Val Phe Arg

305

310

315

320

Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met Ser Lys Val Arg

325

330

335

Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys Phe Leu Met Leu

340

345

350

Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe Phe Ile Val Ser

355

360

365

Gln Val Thr Glu Gly His Trp Lys Trp Gly Gly Ile Thr Val Gln Val

370

375

380

Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp Asn Leu Tyr Val

385

390

395

400

Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys Asn Tyr Gly Glu

405

410

415

Asp Gln Ser Asn Gly Met Gln Leu Pro Cys Lys Ser Arg Glu Asp Cys

420

425

430

Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe Ser Ala Ser Lys

435

440

445

Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

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<213> Homo sapiens

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agaaaggagg cgaggaagga gggagtgtat gagaggagg agcaaaaagc tcaccctaaa 180

acatttatatt caaggagaaa agaaaaaggg ggggcgcaaa aatggctggg gcaattatag 240

aaaacatgag caccaagaag ctgtgcattg ttggtgggat tctgctcgtg ttccaaatca 300

tgccttttct ggtgggaggc ttgattgctc cagggccac aacggcagtg tectacatgt 360

cggtgaaatg tgtgg atg ccc gta aga acc atc aca aga caa aat ggt tgc 411

Met Pro Val Arg Thr Ile Thr Arg Gln Asn Gly Ser

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tgc ctt ggg gac cca atc att gtg aca aga tcc gag aca ttg aag agg 459

Cys Leu Gly Asp Pro Ile Ile Val Thr Arg Ser Glu Thr Leu Lys Arg

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caa ttc caa ggg aaa ttg aag cca atg aca tgc tgt ttt ctg ttc aca 507

Gln Phe Gln Gly Lys Leu Lys Pro Met Thr Ser Cys Phe Leu Phe Thr

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35

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ttc ccc tcc ccc atg gac gtt tcc ctg gct tac cgt gat gac gcg ttt 555

Phe Pro Ser Pro Met Asp Val Ser Leu Ala Tyr Arg Asp Asp Ala Phe

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gct gag tgg act gaa atg gcc cat gaa aga gta cca cgg aaa ctc aaa 603

Ala Glu Trp Thr Glu Met Ala His Glu Arg Val Pro Arg Lys Leu Lys

65

70

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tgc acc ttc aca tct ccc aag act cca gag cat gag ggc cgt tac tat 651

Cys Thr Phe Thr Ser Pro Lys Thr Pro Glu His Glu Gly Arg Tyr Tyr

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85

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gaa tgt gat gtc ctt cct ttc atg gaa att ggg tct gtg gcc cat aag 699
 Glu Cys Asp Val Leu Pro Phe Met Glu Ile Gly Ser Val Ala His Lys
 95 100 105

ttt tac ctt tta aac atc cgg ctg cct gtg aat gag aag aag aaa atc 747
 Phe Tyr Leu Leu Asn Ile Arg Leu Pro Val Asn Glu Lys Lys Lys Ile
 110 115 120

aat gtg gga att ggg gag ata aag gat atc cgg ttg gtg ggg atc cac 795
 Asn Val Gly Ile Gly Glu Ile Lys Asp Ile Arg Leu Val Gly Ile His
 125 130 135 140

caa aat gga ggc ttc acc aag gtg tgg ttt gcc atg aag acc ttc ctt 843
 Gln Asn Gly Gly Phe Thr Lys Val Trp Phe Ala Met Lys Thr Phe Leu
 145 150 155

acg ccc agc atc ttc atc att atg gtg tgg tat tgg agg agg atc acc 891
 Thr Pro Ser Ile Phe Ile Ile Met Val Trp Tyr Trp Arg Arg Ile Thr
 160 165 170

atg atg tcc cga ccc cca gtg ctt ctg gaa aaa gtc atc ttt gcc ctt 939
 Met Met Ser Arg Pro Pro Val Leu Leu Glu Lys Val Ile Phe Ala Leu
 175 180 185

ggg att tcc atg acc ttt atc aat atc cca gtg gaa tgg ttt tcc atc 987
 Gly Ile Ser Met Thr Phe Ile Asn Ile Pro Val Glu Trp Phe Ser Ile
 190 195 200

ggg ttt gac tgg acc tgg atg ctg ctg ttt ggt gac atc cga cag ggc 1035

Gly Phe Asp Trp Thr Trp Met Leu Leu Phe Gly Asp Ile Arg Gln Gly
205 210 215 220

atc ttc tat gcg atg ctt ctg tcc ttc tgg atc atc ttc tgt ggc gag 1083
Ile Phe Tyr Ala Met Leu Leu Ser Phe Trp Ile Ile Phe Cys Gly Glu
225 230 235

cac atg atg gat cag cac gag cgg aac cac atc gca ggg tat tgg aag 1131
His Met Met Asp Gln His Glu Arg Asn His Ile Ala Gly Tyr Trp Lys
240 245 250

caa gtc gga ccc att gcc gtt ggc tcc ttc tgc ctc ttc ata ttt gac 1179
Gln Val Gly Pro Ile Ala Val Gly Ser Phe Cys Leu Phe Ile Phe Asp
255 260 265

atg tgt gag aga ggg gta caa ctc acg aat ccc ttc tac agt atc tgg 1227
Met Cys Glu Arg Gly Val Gln Leu Thr Asn Pro Phe Tyr Ser Ile Trp
270 275 280

act aca gac att gga aca gag ctg gcc atg gcc ttc atc atc gtg gct 1275
Thr Thr Asp Ile Gly Thr Glu Leu Ala Met Ala Phe Ile Ile Val Ala
285 290 295 300

gga atc tgc ctc tgc ctc tac ttc ctg ttt cta tgc ttc atg gta ttt 1323
Gly Ile Cys Leu Cys Leu Tyr Phe Leu Phe Leu Cys Phe Met Val Phe
305 310 315

cag gtg ttt cgg aac atc agt ggg aag cag tcc agc ctg cca gct atg 1371
Gln Val Phe Arg Asn Ile Ser Gly Lys Gln Ser Ser Leu Pro Ala Met

320

325

330

agc aaa gtc cgg cgg cta cac tat gag ggg cta att ttt agg ttc aag 1419

Ser Lys Val Arg Arg Leu His Tyr Glu Gly Leu Ile Phe Arg Phe Lys

335

340

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ttc ctc atg ctt atc acc ttg gcc tgc gct gcc atg act gtc atc ttc 1467

Phe Leu Met Leu Ile Thr Leu Ala Cys Ala Ala Met Thr Val Ile Phe

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ttc atc gtt agt cag gta acg gaa ggc cat tgg aaa tgg ggc ggc atc 1515

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365

370

375

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aca gtc caa gtg aac agt gcc ttt ttc aca ggc atc tat ggg atg tgg 1563

Thr Val Gln Val Asn Ser Ala Phe Phe Thr Gly Ile Tyr Gly Met Trp

385

390

395

aat ctg tat gtc ttt gct ctg atg ttc ttg tat gca cca tcc cat aaa 1611

Asn Leu Tyr Val Phe Ala Leu Met Phe Leu Tyr Ala Pro Ser His Lys

400

405

410

aac tat gga gaa gac cag tcc aat gga atg caa ctc cca tgt aaa tcg 1659

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agg gaa gat tgt gct ttg ttt gtt tcg gaa ctt tat caa gaa ttg ttc 1707

Arg Glu Asp Cys Ala Leu Phe Val Ser Glu Leu Tyr Gln Glu Leu Phe

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agc gct tgc aaa tat tcc ttc atc aat gac aac gca gct tct ggt att 1755

Ser Ala Ser Lys Tyr Ser Phe Ile Asn Asp Asn Ala Ala Ser Gly Ile

445

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460

tgagtcaaca aggcaacaca tgtttatcag ctttgcatTT gcagttgtca cagtcacatt 1815

gattgtactt gtatacgcac acaaatacac tcatttagcc tttatctcaa aatgttaaT 1875

ataaggaaaa aagcgtcaac aataaatatt ctttgagtat tgtc

1919

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<211> 183

<212> PRT

<213> Homo sapiens

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Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

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30

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

55

60

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr
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Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu
85 90 95

Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val
100 105 110

Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn
115 120 125

Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ser
130 135 140

Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala
145 150 155 160

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atg aag ctc tta tct ttg gtg gct gtg gtc ggg tgt ttg ctg gtg ccc 167

Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val Pro

1

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cca gct gaa gcc aac aag agt tct gaa gat atc cgg tgc aaa tgc atc 215

Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys Cys Ile

20

25

30

tgt cca cct tat aga aac atc agt ggg cac att tac aac cag aat gta 263

Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn Gln Asn Val

35

40

45

tcc cag aag gac tgc aac tgc ctg cac gtg gtg gag ccc atg cca gtg 311

Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu Pro Met Pro Val

50

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60

cct ggc cat gac gtg gag gcc tac tgc ctg ctg tgc gag tgc agg tac 359

Pro Gly His Asp Val Glu Ala Tyr Cys Leu Leu Cys Glu Cys Arg Tyr

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Glu Glu Arg Ser Thr Thr Thr Ile Lys Val Ile Ile Val Ile Tyr Leu			
85	90	95	
tcc gtg gtg ggt gcc ctg ttg ctc tac atg gcc ttc ctg atg ctg gtg 455			
Ser Val Val Gly Ala Leu Leu Leu Tyr Met Ala Phe Leu Met Leu Val			
100	105	110	
gac cct ctg atc cga aag ccg gat gca tat act gag caa ctg cac aat 503			
Asp Pro Leu Ile Arg Lys Pro Asp Ala Tyr Thr Glu Gln Leu His Asn			
115	120	125	
gag gag gag aat gag gat gct cgc tct atg gca gca gct gct gca tcc 551			
Glu Glu Glu Asn Glu Asp Ala Arg Ser Met Ala Ala Ala Ala Ala Ser			
130	135	140	
ctc ggg gga ccc cga gca aac aca gtc ctg gag cgt gtg gaa ggt gcc 599			
Leu Gly Gly Pro Arg Ala Asn Thr Val Leu Glu Arg Val Glu Gly Ala			
145	150	155	160
cag cag cgg tgg aag ctg cag gtg cag gag cag cgg aag aca gtc ttc 647			
Gln Gln Arg Trp Lys Leu Gln Val Gln Glu Gln Arg Lys Thr Val Phe			
165	170	175	
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Asp Arg His Lys Met Leu Ser			
180			

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atctgaacac cacagccct gtacttgggt tgcctcttgt cctgaactt cgttgtacca 1478

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1562

<210> 151

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Primer

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<223> Description of Artificial Sequence:Primer

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【配列表フリーテキスト】

配列番号 1 5 1 及び 1 5 2 : プライマー

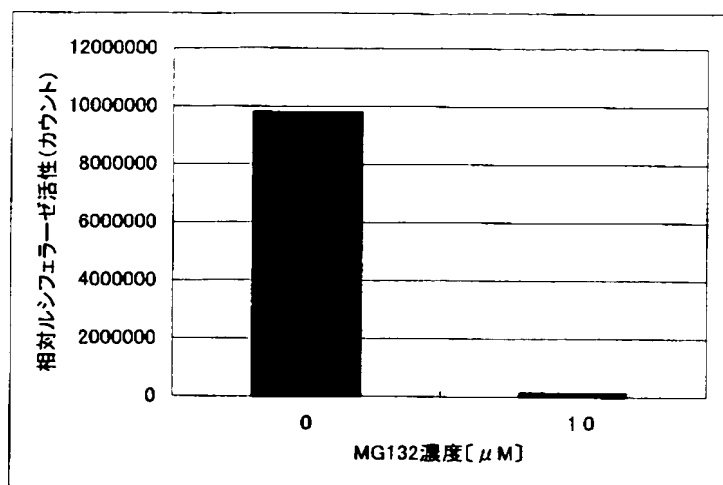
【図面の簡単な説明】

【図 1】

図 1 は、実施例 3 のプロテアソーム阻害剤 MG 1 3 2 による NF- κ B のレポーター活性抑制を示す図である。図中で横軸は、MG 1 3 2 濃度、縦軸は、相対ルシフェラーゼ活性を示す。

【書類名】 図面

【図 1】



【書類名】 要約書

【要約】

【課題】 NF- κ B の過剰な活性化または阻害が関与する疾患の診断、治療または予防等 to 使用される NF- κ B 作用を有するタンパク質の提供。

【解決手段】 ヒト肺線維芽細胞から作製した cDNA ライブラリーから、プラスミド pNF κ B-Luc を用いて、NF- κ B を活性化する作用を有するタンパク質をコードする cDNA をクローニングして、その DNA 配列およびそれより推定されるアミノ酸配列を決定した。同タンパク質、これをコードする DNA、同 DNA を含有する組換えベクターおよび同組換えベクターを含有する形質転換体は、NF- κ B の活性化を阻害または作動する物質のスクリーニングに使用される。

【選択図】 なし

出 願 人 履 歴 情 報

識別番号 [000000033]

1. 変更年月日	2001年 1月 4日
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氏 名	旭化成株式会社